

**THE UNIVERSITY OF CHICAGO**

(i) APPLICANT: Sims, Peter J.

(ii) TITLE OF INVENTION: Compositions and Methods to Inhibit the C5b-9 Complex of Complement

(iii) NUMBER OF SEQUENCES: 18

~~(iv) CORRESPONDENCE ADDRESS:~~

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(C) CITY: Atlanta

(D) STATE: GA

(E) COUNTRY: USA

(F) ZIP: 30309-3450

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US

(B) FILING DATE: 03-FEB-1998

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 31,284

(C) REFERENCE/DOCKET NUMBER: OMRE/170

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear
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## (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ile Gln Gly Gly ~~Ser~~ Val Leu Phe Gly Leu Leu Leu Val Leu Ala  
1 5 10 15

Val Phe Cys His Ser Gly His Ser Leu Gln Cys Tyr Asn Cys Pro Asn  
20 25 30

Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp  
35 40 45

Ala Cys Leu/Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp  
50 55 60

Lys Phe ~~Glu~~ His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu  
65 70 75 80

Asn ~~Glu~~ Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn  
85 90 95

Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu  
 100 105 110

Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro  
 115 120 125

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Rabbit
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ser Arg Gly Val His Leu Leu Leu Arg Leu Leu Phe Leu Leu  
 1 5 10 15

Ala Val Phe Tyr Ser Ser Asp Ser Ser Leu Met Cys Tyr His Cys Leu  
 20 25 30

Leu Pro Ser Pro Asn Cys Ser Thr Val Thr Asn Cys Thr Pro Asn His  
 35 40 45

Asp Ala Cys Leu Thr Ala Val Ser Gly Pro Arg Val Tyr Arg Gln Cys  
 50 55 60

Trp Arg Tyr Glu Asp Cys Asn Phe Glu Phe Ile Ser Asn Arg Leu Glu  
 65 70 75 80

Glu Asn Ser Leu Lys Tyr Asn Cys Cys Arg Lys Asp Leu Cys Asn Gly  
 85 90 95

Pro Glu Asp Asp Gly Thr Ala Leu Thr Gly Arg Thr Val Leu Leu Val  
 100 105 110

Ala Pro Leu Leu Ala Ala Ala Arg Asn Leu Cys Leu  
 115 120

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala  
 1 5 10 15

Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly  
 20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn  
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys  
50 55 60

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Baboon
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Thr Asn Cys Lys Thr Ala  
1 5 10 15

Ile Asn Cys Ser Ser Gly Phe Asp Thr Cys Leu Ile Ala Arg Ala Gly  
20 25 30

Leu Gln Val Tyr Asn Gln Cys Trp Lys Phe Ala Asn Cys Asn Phe Asn  
35 40 45

Asp Ile Ser Thr Leu Leu Lys Glu Asn Glu Leu Gln Tyr Phe Cys Cys  
50 55 60

Lys Glu Asp Leu Cys Asn Glu Gln Leu Glu Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: African green monkey
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Thr Asp Cys Lys Thr Ala  
1 5 10 15

Ile Asn Cys Ser Ser Gly Phe Asp Thr Cys Leu Ile Ala Arg Ala Gly  
20 25 30

Leu Gln Val Tyr Asn Gln Cys Trp Lys Phe Ala Asn Cys Asn Phe Asn  
35 40 45

Asp Ile Ser Thr Leu Leu Lys Glu Ser Glu Leu Gln Tyr Phe Cys Cys  
50 55 60

Figure 1 consists of 16 micrographs arranged in a 4x4 grid. The rows represent different treatments: Control, 100% NaOH, 100% H<sub>2</sub>O<sub>2</sub>, and 100% HCl. The columns represent time points: 0, 1, 2, and 4 hours. Each micrograph shows a petri dish with a lawn of bacterial growth. The control shows increasing growth over time. The 100% NaOH treatment shows no growth at any time point. The 100% H<sub>2</sub>O<sub>2</sub> and 100% HCl treatments show growth at 0 and 1 hour, but no growth at 2 and 4 hours.

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**SECRET**

(2) INFORMATION FOR SEO ID NO:9:

(2) INFORMATION FOR SEO ID NO:10:

506015.1



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mouse
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Leu Thr Cys Tyr His Cys Phe Gln Pro Val Val Ser Ser Cys Asn Met
1          5          10          15
Asn Ser Thr Cys Ser Pro Asp Gln Asp Ser Cys Leu Tyr Ala Val Ala
20          25          30
Gly Met Gln Val Tyr Gln Arg Cys Trp Lys Gln Ser Asp Cys His Gly
35          40          45
Glu Ile Ile Met Asp Gln Leu Glu Glu Thr Lys Leu Lys Phe Arg Cys
50          55          60
Cys Gln Phe Asn Leu Cys Asn Lys Ser Asp
65          70

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Leu Tyr Glu Leu Ile Tyr Val Leu Asp Lys Ala Ser Met Lys Arg Lys
1          5          10          15
Gly Val Glu Leu Lys Asp Ile Lys Arg Cys Leu Gly Tyr His Leu Asp
20          25          30
Val Ser Leu Ala Phe Ser Glu Ile Ser Val Gly Ala Glu Phe Asn Lys
35          40          45
Asp Asp Cys Val Lys Arg Gly Glu Gly Arg Ala Val Asn Ile Thr Ser
50          55          60
Glu Asn Leu Ile Asp Asp Val Val Ser Leu Ile Arg Gly Gly Thr Arg
65          70          75          80
Lys Tyr

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

**060907Z**

Gly Gly Thr Gln Lys Phe  
85

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly Pro Arg Val Tyr Arg Gln Cys  
35 40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid



- (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Cys Leu Gly Tyr His Leu Asp Val Ser Leu Ala Phe Ser Glu Ile  
 1 5 10 15

Ser Val Gly Ala Glu Phe Asn Lys Asp Asp Cys  
 20 25

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